

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

(without alignments)
9956.972 million cell updates/sec

...aaagggtcgtcgaaccca 554

residues

imeters: 4109280

09356766
ATech Paper 1013

Result No.	Score	Query Match	Length	DB	ID	Description
1	554	100.0	9811	10	RNSOD2	X56600 Rat Sod-2-g
2	538.4	97.2	164379	2	AC1089554	AC108955 Rattus no
3	325.4	58.7	203949	10	AL5898878	AL5898878 Mouse DN
4	325.4	58.7	208568	2	AC1271772	AC1271772 Mus muscu
5	318.8	57.5	684	10	MUSMNSOD02	MUSMNSOD02 Mus muscu
6	214.2	38.7	2110	10	AF003694	AF003694 Mus muscu
7	194.8	35.2	396	10	S7883252	S7883252 Mus muscu
8	145.8	26.3	110000	2	AC074222-1	AC074222-1 Mus muscu
9	145.8	26.3	110000	2	AC074222-2	AC074222-2 Mus muscu
10	130.2	23.5	110000	2	AC074222-1	AC074222-1 Mus muscu
11	116	20.9	1438	10	RNMSNSOD	RNMSNSOD Mus muscu
12	116	20.9	1492	6	AX401951	AX401951 Rat mRNA
13	108.6	19.6	487	9	HUMMSDA	HUMMSDA Homo sapien
14	108.6	19.6	165802	9	AL135914	AL135914 Human DN
15	108	19.5	836	10	BC018173	BC018173 Mus muscu
16	108	19.5	1162	10	BC010548	BC010548 Mus muscu
17	106.4	19.2	779	10	MNMSODRX	MNMSODRX Mus muscu
18	106.4	19.2	897	10	MNMSODR	MNMSODR Mus muscu
19	105.8	19.1	12857	9	S77127	S77127 Mouse mRNA
20	100.2	18.1	627	6	EB08014	EB08014 Homo-sapien
21	100.2	18.1	969	6	AR054016	AR054016 Homo-sapien
22	100.2	18.1	969	6	AR146192	AR146192 Sequence
23	100.2	18.1	969	9	HSMNSODDE	HSMNSODDE Sequence
24	100.2	18.1	989	9	HSMNSUDIS	HSMNSUDIS Sequence
25	100	18.1	324	6	AX397183	AX397183 Human mRNA
26	100	18.1	522	6	AL12179	AL12179 H.sapiens m
27	100	18.1	535	6	AL12178	AL12178 H.sapiens m
28	100	18.1	600	6	AL12180	AL12180 Artificial
29	100	18.1	600	6	AL12190	AL12190 Artificial
30	100	18.1	600	6	AL12191	AL12191 Artificial
31	100	18.1	600	6	AL12200	AL12200 Nucleotide
32	100	18.1	603	6	AL12233	AL12233 H.sapiens m
33	100	18.1	627	6	EB08013	EB08013 DNA encodin
34	100	18.1	813	6	AR066849	AR066849 Sequence
35	100	18.1	813	6	AR106627	AR106627 Sequence
36	100	18.1	813	6	ES01408	ES01408 Human mRNA
37	100	18.1	829	9	HSMNSODR	HSMNSODR Homo sapi
38	100	18.1	940	6	BC012423	BC012423 Homo sapi
39	100	18.1	1026	6	AX134340	AX134340 Sequence
40	100	18.1	1026	9	HSSOD	HSSOD Human mRNA
41	100	18.1	2555	9	AK097395	AK097395 Homo sapi
42	98.4	17.8	594	6	AR130379	AR130379 Sequence
43	98.4	17.8	609	6	ES03557	ES03557 Synthetic D
44	98.4	17.8	633	10	CPU39843	CPU39843 Cavia porce
45	98.4	17.8	681	6	AR130381	AR130381 Sequence

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a

RESULT 1				
RNSOD2				
LOCUS	RNSOD2	9811 bp	DNA	
DEFINITION	Rat SOD-2 gene for manganese-containing superoxide dismutase.			
ACCESSION	X56600			linear
VERSION	X56600.1	GI:57272		12-SEP-1996
KEYWORDS	SOD2 gene; superoxide dismutase.			
SOURCE	Rattus norvegicus.			
ORGANISM	Rattus norvegicus			
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			
	Rattus.			
REFERENCE	1 (bases 1 to 9811)			
AUTHORS	Ho, Y.S.			
TITLE	Direct Submission			

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2003, 04:23:52 ; Search time 1362.05 Seconds

(without alignments)
9956.972 Million cell updates/sec

Title: US-09-856-766-2

Perfect score: 466

Sequence: 1 cgttagcgggttcgacaaag.....ttacttgcgaatcagagcc 466

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBank:*

1: gb_ba:*

2: gb_hcg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_srs:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: gb_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_ov:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_srs:*

28: em_un:*

29: em_vl:*

30: em_hcg_hum:*

31: em_hcg_inv:*

32: em_hcg_other:*

33: em_hcg_mus:*

34: em_hcg_pln:*

35: em_hcg_rod:*

36: em_hcg_mam:*

37: em_hcg_vtc:*

38: em_sy:*

39: em_hgo_hum:*

40: em_hgo_mus:*

41: em_hgo_other:*

09856768
ATTACH
PAPW NO 13

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	466	100.0	12857	9 S77127	S77127 Homo sapien
2	464.4	99.7	1984	9 HSM800535	AL050388 Homo sapi
3	464.4	99.7	165802	9 AL135914	AL135914 Human DNA
4	247	53.0	1617	9 BC016934	BC016934 Homo sapi
5	98.6	21.2	203949	10 AL589878	AL589878 Mouse DNA
6	98.6	21.2	208568	2 AC127172	AC127172 Mus muscu
7	98	21.0	2110	10 AF003694	AF003694 Mus muscu
8	97	20.8	684	10 MUSMNSD02	L35526 Mus musculu
9	93	20.0	164373	2 AC108954	AC108954 Rattus no
10	91	19.5	9811	10 RNSOD2	X56600 Rat SOD-2 g
11	72.2	15.5	110000	2 AC074222_1	Continuation (2 of
12	46.8	10.0	146383	2 AC116367	AC116367 Oryza sat
13	45.8	9.8	27263	2 AC106990	AC106990 Rattus no
14	44	9.4	150312	9 CNS01R1J	AL163613 Human chr
15	44	9.4	151171	2 AC020775	AC020775 Homo sapi
16	44	9.4	185636	2 AC027109	AC027109 Homo sapi
17	43.2	9.3	16258	6 AX348424	AX348424 Sequence
18	43.2	9.3	16258	6 AX348807	AX348807 Sequence
19	43	9.2	4904	9 AB037804	AB037804 Homo sapi
20	43	9.2	98078	9 AL451083	AL451083 Human DNA
21	43	9.2	157918	2 AL360019	AL360019 Homo sapi
22	43	9.2	158255	2 AC025695	AC025695 Homo sapi
23	42.8	9.2	172210	9 AC098656	AC098656 Homo sapi
24	42.6	9.1	135961	2 AC0021288	AC0021288 Homo sapi
25	42.6	9.1	149378	9 AC008708	AC008708 Homo sapi
26	42.4	9.1	167667	9 AC009329	AC009329 Homo sapi
27	42.4	9.1	180359	2 AC022064	AC022064 Homo sapi
28	42.2	9.1	28326	3 AC024808	AC024808 Caenorhab
29	42.2	9.0	17848	6 AX277865	AX277865 Sequence
30	42	9.0	17848	6 AX323550	AX323550 Sequence
31	42	9.0	17848	6 AX348363	AX348363 Sequence
32	42	9.0	17848	6 AC094710	AC094710 Rattus no
33	41.8	8.9	167500	2 AC094601	AX346041 Sequence
34	41.6	8.9	5678	6 AC006532	AC006532 Arabidops
35	41.4	8.9	76976	8 AC0097950	AC0097950 Rattus no
36	41.4	8.9	158832	2 AL592045	AL592045 Homo sapi
37	41.4	8.9	181719	2 AC122856	AC122856 Mus muscu
38	41.4	8.9	191233	2 AC021883	AC021883 Homo sapi
39	41.4	8.9	232180	2 HSDJ47M23	AL096816 Human DNA
40	41.2	8.8	129320	9 AC078838	AC078838 Homo sapi
41	41.2	8.8	148116	2 AC083801	AC083801 Homo sapi
42	41.2	8.8	159621	9 AC073950	AC073950 Homo sapi
43	41.2	8.8	174040	2 AC125492	AC125492 Homo sapi
44	41	8.8	105400	9 AL357352	AL357352 Human DNA
45	41	8.8	106601	9	

ALIGNMENTS

RESULT 1

S77127 12857 bp DNA linear PRI 05-JUN-2000

LOCUS Homo sapiens manganese superoxide dismutase gene, complete cds.

DEFINITION S77127

ACCESSION S77127.1 GI:998582

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens.

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

Wan,X.S., Devalaraja,M.N. and St Clair,D.K.

1 (bases 1 to 12857)

AUTHORS

Molecular structure and organization of the human manganese superoxide dismutase gene